SEQUENCE LISTING

<110> BML, INC.

<120> Method of Detecting Risk Factor for Onset of Diabetes

<130> PBM37

<140>
<141>

<160> 23

<170> PatentIn Ver. 2.0

<210> 1
<211> 1305
<212> DNA
<213> Hominidae

<220>
<221> CDS
<222> (1)..(900)

<400> 1

-103 aaa cagaagggga ggtgcagttt cagaacccag ccagcctctc -61

tcttgctgcc tagcctcctg ccggcctcat cttcgcccag ccaaccccgc ctggagccct -1

atg gcc aac tgc gag ttc agc ccg gtg tcc ggg gac aaa ccc tgc tgc 48
Met Ala Asn Cys Glu Phe Ser Pro Val Ser Gly Asp Lys Pro Cys Cys
1 5 10 15

cgg ctc tct agg aga gcc caa ctc tgt ctt ggc gtc agt atc ctg gtc 96
Arg Leu Ser Arg Arg Ala Gln Leu Cys Leu Gly Val Ser Ile Leu Val
20 25 30

ctg atc ctc gtc gtg gtg ctc gcg gtg gtc gtc ccg agg tgg cgc cag 144
Leu Ile Leu Val Val Val Leu Ala Val Val Val Pro Arg Trp Arg Gln
35 40 45

cag tgg agc ggt ccg ggc acc acc aag cgc ttt ccc gag acc gtc ctg 192
Gln Trp Ser Gly Pro Gly Thr Thr Lys Arg Phe Pro Glu Thr Val Leu
50 55 60

gcg cga tgc gtc aag tac act gaa att cat cct gag atg aga cat gta 240

Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro Glu Met Arg His Val
65 70 75 80

gac tgc caa agt gta tgg gat gct ttc aag ggt gca ttt att tca aaa 288
Asp Cys Gln Ser Val Trp Asp Ala Phe Lys Gly Ala Phe Ile Ser Lys
85 90 95

cat cct tgc aac att act gaa gaa gac tat cag cca cta atg aag ttg 336
His Pro Cys Asn Ile Thr Glu Glu Asp Tyr Gln Pro Leu Met Lys Leu
100 105 110

gga act cag acc gta cct tgc aac aag att ctt ctt tgg agc aga ata 384
Gly Thr Gln Thr Val Pro Cys Asn Lys Ile Leu Leu Trp Ser Arg Ile
115 120 125

aaa gat ctg gcc cat cag ttc aca cag gtc cag cgg gac atg ttc acc 432
Lys Asp Leu Ala His Gln Phe Thr Gln Val Gln Arg Asp Met Phe Thr
130 135 140

ctg gag gac acg ctg cta ggc tac ctt gct gat gac ctc aca tgg tgt 480
Leu Glu Asp Thr Leu Leu Gly Tyr Leu Ala Asp Asp Leu Thr Trp Cys
145 150 155 160

ggt gaa ttc aac act tcc aaa ata aac tat caa tct tgc cca gac tgg 528
Gly Glu Phe Asn Thr Ser Lys Ile Asn Tyr Gln Ser Cys Pro Asp Trp
165 170 175

aga aag gac tgc agc aac aac cct gtt tca gta ttc tgg aaa acg gtt 576
Arg Lys Asp Cys Ser Asn Asn Pro Val Ser Val Phe Trp Lys Thr Val
180 185 190

tcc cgc agg ttt gca gaa gct gcc tgt gat gtg gtc cat gtg atg ctc 624
Ser Arg Arg Phe Ala Glu Ala Ala Cys Asp Val Val His Val Met Leu
195 200 205

aat gga tcc cgc agt aaa atc ttt gac aaa aac agc act ttt ggg agt 672
Asn Gly Ser Arg Ser Lys Ile Phe Asp Lys Asn Ser Thr Phe Gly Ser
210 215 220

gtg gaa gtc cat aat ttg caa cca gag aag gtt cag aca cta gag gcc 720
Val Glu Val His Asn Leu Gln Pro Glu Lys Val Gln Thr Leu Glu Ala
225 230 235 240

tgg gtg ata cat ggt gga aga gaa gat tcc aga gac tta tgc cag gat 768
Trp Val Ile His Gly Gly Arg Glu Asp Ser Arg Asp Leu Cys Gln Asp
245 250 255

ccc acc ata aaa gag ctg gaa tcg att ata agc aaa agg aat att caa 816
Pro Thr Ile Lys Glu Leu Glu Ser Ile Ile Ser Lys Arg Asn Ile Gln

```
            260                 265                 270

ttt tcc tgc aag aat atc tac aga cct gac aag ttt ctt cag tgt gtg   864
Phe Ser Cys Lys Asn Ile Tyr Arg Pro Asp Lys Phe Leu Gln Cys Val
        275                 280                 285

aaa aat cct gag gat tca tct tgc aca tct gag atc tgagccagtc        910
Lys Asn Pro Glu Asp Ser Ser Cys Thr Ser Glu Ile
    290                 295                 300

gctgtggttg ttttagctcc ttgactcctt gtggtttatg tcatcataca tgactcagca 970

tacctgctgg tgcagagctg aagattttgg agggtcctcc acaataaggt caatgccaga 1030

gacggaagcc tttttcccca aagtcttaaa ataacttata tcatcagcat acctttattg 1090

tgatctatca atagtcaaga aaaattattg tataagatta gaatgaaaat tgtatgttaa 1150

gttacttcac tttaattctc atgtgatcct tttatgttat ttatatattg gtaacatcct 1210

ttctattgaa aaatcaccac accaaacctc tcttattaga acaggcaagt gaagaaaagt 1270

gaatgctcaa gtttttcaga aagcattaca tttcc                            1305
```

<210> 2
<211> 300
<212> PRT
<213> Hominidae

<400> 2

```
Met Ala Asn Cys Glu Phe Ser Pro Val Ser Gly Asp Lys Pro Cys Cys
  1               5                  10                  15

Arg Leu Ser Arg Arg Ala Gln Leu Cys Leu Gly Val Ser Ile Leu Val
             20                  25                  30

Leu Ile Leu Val Val Val Leu Ala Val Val Val Pro Arg Trp Arg Gln
         35                  40                  45

Gln Trp Ser Gly Pro Gly Thr Thr Lys Arg Phe Pro Glu Thr Val Leu
     50                  55                  60

Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro Glu Met Arg His Val
 65                  70                  75                  80

Asp Cys Gln Ser Val Trp Asp Ala Phe Lys Gly Ala Phe Ile Ser Lys
                 85                  90                  95
```

```
His Pro Cys Asn Ile Thr Glu Glu Asp Tyr Gln Pro Leu Met Lys Leu
            100                 105                 110

Gly Thr Gln Thr Val Pro Cys Asn Lys Ile Leu Leu Trp Ser Arg Ile
        115                 120                 125

Lys Asp Leu Ala His Gln Phe Thr Gln Val Gln Arg Asp Met Phe Thr
    130                 135                 140

Leu Glu Asp Thr Leu Leu Gly Tyr Leu Ala Asp Asp Leu Thr Trp Cys
145                 150                 155                 160

Gly Glu Phe Asn Thr Ser Lys Ile Asn Tyr Gln Ser Cys Pro Asp Trp
                165                 170                 175

Arg Lys Asp Cys Ser Asn Asn Pro Val Ser Val Phe Trp Lys Thr Val
            180                 185                 190

Ser Arg Arg Phe Ala Glu Ala Ala Cys Asp Val Val His Val Met Leu
        195                 200                 205

Asn Gly Ser Arg Ser Lys Ile Phe Asp Lys Asn Ser Thr Phe Gly Ser
    210                 215                 220

Val Glu Val His Asn Leu Gln Pro Glu Lys Val Gln Thr Leu Glu Ala
225                 230                 235                 240

Trp Val Ile His Gly Gly Arg Glu Asp Ser Arg Asp Leu Cys Gln Asp
                245                 250                 255

Pro Thr Ile Lys Glu Leu Glu Ser Ile Ile Ser Lys Arg Asn Ile Gln
            260                 265                 270

Phe Ser Cys Lys Asn Ile Tyr Arg Pro Asp Lys Phe Leu Gln Cys Val
        275                 280                 285

Lys Asn Pro Glu Asp Ser Ser Cys Thr Ser Glu Ile
    290                 295                 300
```

<210> 3
<211> 61
<212> DNA
<213> Hominidae

<400> 3
cgcccgccgc gccccgcgcc cgtcccgccg cccccgcccg atcttcgccc agccaacccc 60

g 61

<210> 4
<211> 21
<212> DNA
<213> Hominidae

<400> 4
accggtgcgc cttagtcgcc a 21

<210> 5
<211> 21
<212> DNA
<213> Hominidae

<400> 5
tagactgcat gttagacgag a 21

<210> 6
<211> 62
<212> DNA
<213> Hominidae

<400> 6
cgcccgccgc gccccgcgcc cgtcccgccg cccccgcccg tttggaccta tgaattgtta 60

cc 62

<210> 7
<211> 21
<212> DNA
<213> Hominidae

<400> 7
gacatgctaa attgatctca g 21

<210> 8
<211> 60
<212> DNA
<213> Hominidae

<400> 8
cgcccgccgc gccccgcgcc cgtcccgccg cccccgcccg cagcagaagt cactctgttc 60

<210> 9
<211> 21
<212> DNA
<213> Hominidae

<400> 9
ccattctcca gcctccgtct t 21

<210> 10
<211> 62
<212> DNA
<213> Hominidae

<400> 10
cgcccgccgc gccccgcgcc cgtcccgccg cccccgcccg caagcactga ctgagtaacg 60

tc 62

<210> 11
<211> 22
<212> DNA
<213> Hominidae

<400> 11
aaactgctgg aggatggtga tt 22

<210> 12
<211> 63
<212> DNA
<213> Hominidae

<400> 12
cgcccgccgc gccccgcgcc cgtcccgccg cccccgcccg ttcactgtga tatttgcaac 60

agg 63

<210> 13
<211> 23
<212> DNA
<213> Hominidae

<400> 13
ggttgatgtt tggggttctt tgt 23

<210> 14
<211> 64
<212> DNA
<213> Hominidae

<400> 14
cgcccgccgc gccccgcgcc cgtcccgccg cccccgcccg tgtggattct tttgtggact 60

gatt 64

<210> 15
<211> 61
<212> DNA
<213> Hominidae

<400> 15
cgcccgccgc gccccgcgcc cgtcccgccg cccccgcccg ttgtccaggg cgtgctacaa 60

a 61

<210> 16
<211> 21
<212> DNA
<213> Hominidae

<400> 16
agattcacac agccctccaa g 21

<210> 17
<211> 62
<212> DNA
<213> Hominidae

<400> 17
cgcccgccgc gccccgcgcc cgtcccgccg cccccgcccg ttagcgaatt ggacgacaga 60

tg 62

<210> 18
<211> 22
<212> DNA
<213> Hominidae

<400> 18
tctggcattg accttattgt gg 22

<210> 19
<211> 22
<212> DNA
<213> Hominidae

<400> 19
ctccgccact ctcctgcaca ca 22

<210> 20
<211> 20
<212> DNA
<213> Hominidae

<400> 20
gggcctccag cagaagtcac 20

<210> 21
<211> 21
<212> DNA
<213> Hominidae

<400> 21
ttgtccaggg cgtgctacaa a 21

<210> 22
<211> 66
<212> DNA
<213> Hominidae

<400> 22
ttagcgaatt ggacgacaga tgtatcctac ggtctcttga tttccttttt tgctttcttg 60

tcatag 66